

QY 301 CCGGAGTGACCCCTTCTACACCTATCCGCTGGCCATCCGCTGTGACCTGGAGCCCTG 360
 DB 416 CCGGAGTGACCCCTTCTACACCTATCCGCTGGCCATCCGCTGTGACCTGGAGCCCTG 475
 QY 361 TCCAGTCCACCAAGAGT 379
 DB 476 TCCAGTCCACCAAGAGT 494

RESULT 2
 A0495547 405 bp DNA linear GSS 28-APR-1999
 LOCUS HS-5211.B1.H08.SP6E.RPCI-11 Human Male BAC library Homo sapiens
 DEFINITION genomic clone Plate=787 Col=15 Row=P, DNA sequence.
 ACCESSION A0495547
 VERSION A0495547.1 GI:4695670
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 405)
 Mahatras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,Y.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.
 Sequencing tagged connectors: A sequence approach to mapping and
 scanning the human genome
 Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
 99380589
 Contact: Mahatras GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@jeng.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
 or from Resear h Genetics (info@resgen.com). BAC end Web Server:
 http://www.htsc.washington.edu
 Plate: 787 row: P column: 15
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 405.

FEATURES
 Source Location/Qualifiers
 1..405
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate=787 Col=15 Row=P"
 /clone_lib="RPCI-11 Human Male BAC Library"
 /sex="male"
 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBACe3.6 vector at EcoRI sites"

BASE COUNT 97 a 126 c 89 g 93 t
 ORIGIN
 Query Match 48.2%; Score 188; DB 12; Length 405;
 Best Local Similarity 100.0%; Pred. No. 1.2e-37;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 203 AGAAGCCATTTGTGACACCCCTATATGAGCCCATCATGAGCTGTACTACACAG 262
 DB 22 AGAAGCCATTTGTGACACCCCTATATGAGCCCATCATGAGCTGTACTACACAG 81
 QY 263 AGACCAACAGAGTGTGACAGCTGCCCACTGTGCCCCGGGAGTGCACCCCTTCTACA 322
 DB 82 AGACCAACAGAGTGTGACAGCTGCCCACTGTGCCCCGGGAGTGCACCCCTTCTACA 141

QY 323 CCTATCCCGTGGCCATCCGCTGTGACTGCGAGACCTGCTCCACTCCACACAGAGTGTG 382
 DB 142 CCTATCCCGTGGCCATCCGCTGTGACTGCGAGACCTGCTCCACTCCACACAGAGTGTG 201
 QY 383 AGACCATC 390
 DB 202 AGACCATC 209

RESULT 3
 BM262079/c 560 bp mRNA linear EST 18-DEC-2001
 LOCUS dag40d11.x3 Blackshear/Soares normalized Xenopus egg library
 DEFINITION Xenopus laevis cDNA clone IMAGE:4783917 3' similar to SW-GRB-CYPCA
 P01235 GONADOTROPIN BETA CHAIN PRECURSOR. [1] ; mRNA sequence.
 ACCESSION BM262079
 VERSION BM262079.1 GI:17925119
 KEYWORDS EST.
 SOURCE African clawed frog.
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 Xenopodinae; Xenopus.
 1 (bases 1 to 560)
 Clifton,S., Johnson,S.T., Blumberg,B., Song,J., Hillier,L., Pape,D.,
 Martin,J., Wylie,T., Underwood,K., Theisling,B., Bowers,Y., Person
 ,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
 Waterston,R. and Wilson,R.
 WashU Xenopus EST project, 1999
 Unpublished (1999)
 Contact: Sandy Clifton, Ph.D.
 WashU Xenopus EST project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Library constructed by Bento Soares and M. Fatima Bonaldo
 (University of Iowa). DNA Sequencing by: Washington University
 Genome Sequencing Center
 Clone distribution: Xenopus clones from this library are available
 through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
 Seq primer: -40UP from G1bc0
 High quality sequence stop: 473.

FEATURES
 Source Location/Qualifiers
 1..560
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone="IMAGE:4783917"
 /clone_lib="Blackshear/Soares normalized Xenopus egg
 library"
 /sex="female"
 /tissue="type="unfertilized egg"
 /cell_type="unfertilized egg"
 /dev_stage="unfertilized egg"
 /lab_host="DH10B"
 /note="Vector: pT73-Pac; Site_1: EcoRI; Site_2: NotI;
 polyA-selected mRNA was prepared from unfertilized Xenopus
 laevis eggs. The library was constructed in the vector
 pT73-Pac as described in Bonaldo, M.F., Lennon, G. and
 Soares, M.B. 'Normalization and subcloning: two
 approaches to facilitate gene discovery'. Genome Research
 6:791-806, 1996. The first strand synthesis used a
 NotI-GT18 primer; double stranded cDNAs were ligated to
 EcoRI adapters, digested with NotI, and directionally
 cloned into the NotI and EcoRI-digested pT73-Pac vector.
 The library contained approximately 7.2 x 10⁵
 recombinants, with average insert sizes of 1-1.5 kb."

BASE COUNT 164 a 112 c 120 g 164 t
 ORIGIN
 Query Match 45.3%; Score 176.6; DB 10; Length 560;
 Best Local Similarity 73.0%; Pred. No. 1.1e-34;

QY 164 a 112 c 120 g 164 t